

I. Sticks

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: November 9, 2001, 09:23:38 ; Search time 1561.35 Seconds

(without alignments)  
16454.947 Million cell updates/sec

Title: US-09-001-737-7

Perfect score: 1661  
Sequence: 1 GAATTCGCGTTCATATGCA.....TGGCGCGATAGCCGCAATTC 1661

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba1:\*

2: gb\_ba2:\*

3: gb\_ba3:\*

4: gb\_in1:\*

5: gb\_in2:\*

6: gb\_in3:\*

7: gb\_cm:\*

8: gb\_ov:\*

9: gb\_pat1:\*

10: gb\_pat2:\*

11: gb\_ph:\*

12: gb\_p11:\*

13: gb\_p12:\*

14: gb\_p13:\*

15: gb\_p14:\*

16: em\_ba1:\*

17: em\_ba2:\*

18: em\_fun:\*

19: em\_htgo\_hum:\*

20: em\_htgo\_inv:\*

21: em\_htgo\_rtd:\*

22: em\_htg\_hum1:\*

23: em\_htg\_hum2:\*

24: em\_htg\_hum3:\*

25: em\_htg\_hum4:\*

26: em\_htg\_hum5:\*

27: em\_htg\_hum6:\*

28: em\_htg\_hum7:\*

29: em\_htg\_hum8:\*

30: em\_htg\_hum1:\*

31: em\_htg\_inv1:\*

32: em\_htg\_inv2:\*

33: em\_htg\_other:\*

34: em\_htg\_rtd:\*

35: em\_hum1:\*

36: em\_hum2:\*

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45: em\_pat:\*

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97: gb\_v12:\*

98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1622.2	97.7	10389	1	AE006627
2	1413.4	85.1	2683	3	SPGROEIGN
3	1053.8	63.4	1718	2	AF325222
4	1038.6	62.5	21494	84	SPNENI924
5	1038.4	62.5	1926	10	AX073958
6	1030.6	62.0	2401	1	AF117741
7	955	57.5	12560	1	AE006276
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					X71132 L.lactis gr

9	942.2	56.7	2187	2	AY029215
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11	838.8	50.5	2309	2	BACSGROSL
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13	816.4	49.2	1977	2	AF274871
14	807.4	48.6	2400	2	BACGROESL
15	807.4	48.6	2325	2	BACGROESL
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17	807.4	48.1	213190	2	BSUB0004
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20	786.4	47.3	296950	2	AF001508
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22	771	46.4	2753	2	AF214488
23	756.4	45.5	3985	2	AF269843
24	751.6	45.2	2187	3	SEU13618
25	739.8	44.5	2540	2	D55630
26	726.2	44.3	2675	1	AF031929
27	722.4	43.5	2712	3	STAHSP
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29	688.8	41.5	3987	2	CPGROESL
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34	656.4	39.5	2103	3	TH056021
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40	644.6	38.8	1811	3	LPNHPBC
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42	640.8	38.6	1635	2	BGRROELT
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## ALIGNMENTS

RESULT 1  
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LOCUS Streptococcus pyogenes strain SF370 serotype M1, section 156 of 167  
DEFINITION of the complete genome.  
ACCESSION AE006627 AE004092  
VERSION AE006627.1 GI:13623059  
KEYWORDS  
SOURCE Streptococcus pyogenes.  
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
Streptococcus.

REFERENCE 1 (bases 1 to 10389)  
AUTHORS Ferretti, J.J., McShan, W.M., Adjic, D., Savic, G., Lyon, K.,  
Primeaux, C., Szate, S.S., Surov, A.N., Kenton, S., Lal, H., Lin, S.,  
Yuan, Y., Jia, H.G., Najjar, F.Z., Ren, O., Zhu, H., Song, L., White, J.,  
Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.

TITLE Complete genome sequence of an M1 strain of Streptococcus pyogenes  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)  
MEDLINE 21192684  
PMID 11296236

REFERENCE 2 (bases 1 to 10389)  
AUTHORS Ferretti, J.J., McShan, W.M., Adjic, D., Savic, G., Lyon, K.,  
Primeaux, C., Szate, S.S., Surov, A.N., Kenton, S., Lal, H., Lin, S.,  
Yuan, Y., Jia, H.G., Najjar, F.Z., Ren, O., Zhu, H., Song, L., White, J.,  
Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.

TITLE Direct Submission  
JOURNAL Submitted (10-APR-2001) Department of Microbiology and Immunology,  
University of Oklahoma Health Sciences Center, 940 St Young Blvd,  
Oklahoma City, OK 73104, USA  
FEATURES Location/Qualifiers

source

gene

CDS

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D. A., Whitton, M. M., Rogers, J. and R. A. Vanhogen.
2000. Two-dimensional gel electrophoresis map of
Streptococcus pyogenes proteins. Unpublished data.; Best
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2000. Two-dimensional gel electrophoresis map of
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2000. Two-dimensional gel electrophoresis map of
Streptococcus pyogenes proteins. Unpublished data.; Best
Blastp hit = emb|CA61520.1| (X89236) heat shock protein
[Streptococcus pyogenes]"

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RESULT,	2
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DEFINITION	S. pyogenes DNA for groEL gene.
ACCESSION	X89236
VERSION .	X89236.1 GI:2462691
KEYWORDS	groEL gene; heat shock protein 60 (GroEL) like protein. Streptococcus pyogenes Streptococcus pyogenes Bacteria; Firmicutes; Bacillus/clostridium group; Streptococcaceae Streplococcus
SOURCE	1 (bases 1 to 2683) Podbielski,A.
ORGANISM	Direct Submission
REFERENCE	Submitted (29-JUN-1995). A. Podbielski, Institut f Med
AUTHORS	Microbiologie, an der Rhein Westf. Techn. Hochschule, Aachen,
TITLE	
JOURNAL	

QY	201	GATCATTTTAAACACATGGGAGACAAATTTGGTCTCGAAGTGGCTCTAAACCAATGAT	260
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QY	261	ATTGCTGTATGGGAGACACTACTGCAACAGTTTACACAAAGCCATTGTCATGAAGA	320
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QY	561	ACAGAACCTTGAAGTGGTGAAGCATCAATTTGACCGTGGTTACCTGCTCCAAATACATG	620
Db	361	ACAGAACCTTGAAGTGGTGAAGCATCAATTTGACCGTGGTTACCTGCTCCAAATACATG	420
QY	621	GTCACAGACATGAAGAAAATGGTGTGCAGACCTTGAAGAACCCATTATCTTAATCAGGAT	680
Db	421	GTCACAGACATGAAGAAAATGGTGTGCAGACCTTGAAGAACCCATTATCTTAATTTGGAT	480
QY	681	AAAAAAGTCAACATCCAGACATTTTGGCCACTACTTGTAGAGAGTCTTTAAACCAAC	740

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
1	Jwo-Farn, C	Cloning, sequencing, and characterization of 60 kDa Chaperon from <i>Streptococcus agalactiae</i> unpublished	2 (bases 1 to 1718)	2	Jwo-Farn, C	Direct Submission Submitted (30-NOV-2000) Department of Microbiology, National Taiwan University, Jen-Ai Rd. Section 1, No. 1, Taipei, Taiwan 10018, Republic of China	Location/Qualifiers
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ORIGIN							
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Matches 1269;	Conservative	0;	Mismatches 337;	Indels 3;	Gaps 1;		
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QY	74	TATGTTACAGATACCGTCGAAGTAACGCTTGTCCTAAAGGCGCAATGTTGTTCTTGA	133				
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QY	134	AAAGCTTTGCTTCGCCCTTAAATACAAATGACGGGGGTACCATTTGCTAAAGAGATCGA	193				
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QY	194	ATTGACAGATCATTTTGGAAAAACATGGGACAAATTTGCTGCTGAAGTGCCTTTAAAC	253				
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QY	374	AACAGCAACACACAGCTGTGAAGCTTGAAGGCATTTGCTCAACCTGTATCTGGCA	433				
DB	455	AACACCTTTTCACACAGCTTGAAGACCTTAAAGAGATTTGACACAAGTTTTCAGGCA	514				



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 Oy 494 CTCGAAAGCATGATGAGCGCTGGGCGAAGGATGATGATGATGATGATGATGATGATGAT 553  
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 Oy 554 TATGAAAGCATGATGAGCGCTGGGCGAAGGATGATGATGATGATGATGATGATGATGAT 613  
 Db 7475 TATGAAAGCATGATGAGCGCTGGGCGAAGGATGATGATGATGATGATGATGATGATGAT 7416  
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 VERSION AX073958.1 GI:12710218  
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 ORGANISM artificial sequence.  
 REFERENCE 1 (bases 1 to 1926)  
 AUTHORS Siegel, M., Chu, N.R. and Mizzen, L.A.  
 TITLE Induction of a Th1-like response in vitro  
 JOURNAL Patent: WO 0104344-A 50 18-JAN-2001;  
 Stressgen Biotechnologies Corporation (CA)  
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 BASE COUNT 585 a 382 c 464 g 495 t  
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 Matches 1288; Conservative 0; Mismatches 366; Indels 0; Gaps 0;



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LOCUS AF117741
DEFINITION Streptococcus pneumoniae strain CP1200 co-chaperonin GroES (groES)
and Chaperonin GroEL (groEL) genes, complete cds.
ACCESSION AF117741
VERSION AF117741.1 GI:4566771
KEYWORDS Streptococcus pneumoniae.
SOURCE Streptococcus pneumoniae.
ORGANISM Streptococcus pneumoniae;
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
REFERENCE 1 (bases 1 to 2401)
AUTHORS Kim,S.N., Lee,J.Y., Kim,S.W., Choi,I.H. and Rhee,D.K.
TITLE groEL sequences in Streptococcus pneumoniae
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2401)
AUTHORS Kim,S.N., Kim,S.W., Choi,I.H. and Rhee,D.K.
JOURNAL Direct Submission
Submitted (04-JAN-1999) Pharmacy, Sungkyunkwan University, 300
Chunchun-dong, Suwon, Kyunggi-Do 440-746, Korea
LOCATION/Qualifiers
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2274..2302
terminator 743 a 459 c 568 g 631 t
BASE COUNT
ORIGIN

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Best Local Similarity 77.2% Pred. No. 9.2e-197;
Matches 1252; Conservative 0; Mismatches 369; Indels 0; Gaps 0;

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DEFINITION Lactococcus lactis subsp. lactis IL1403 section 38 of 218 of the complete genome.  
ACCESSION AE006276 AE005176  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 12560)  
AUTHORS Bolotin, A., Mincker, P., Manger, S., Jallion, O., Malarme, K., Weissenbach, J., Ehrlich, S.D. and Sorokin, A.  
TITLE The complete genome sequence of the lactic acid bacterium Lactococcus lactis  
JOURNAL Genome Res. (2001) In press  
REFERENCE 2 (bases 1 to 12560)  
AUTHORS Bolotin, A., Mincker, P., Manger, S., Jallion, O., Malarme, K., Weissenbach, J., Ehrlich, S.D. and Sorokin, A.  
TITLE Direct submission  
JOURNAL Submitted (09-JAN-2001) INRA, Genetique Microbienne, Domaine de Vilvert, Jouy en Josas 78352, France  
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RESULT 8
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DEFINITION L.lactis groes and groEL genes.
ACCESSION X71132
VERSION X71132.1 GI:287869
KEYWORDS groEL gene; groes gene; heat shock protein.
SOURCE Lactococcus lactis.
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Lactococcus.
REFERENCE 1 (bases 1 to 2267)
AUTHORS Kim, S.G. and Batt, C.A.
TITLE Cloning and sequencing of the Lactococcus lactis subsp. lactis. .
JOURNAL Gene in press
AUTHORS 2 (bases 1 to 2267)
Batt, C.A.
DIRECT SUBMISSION
SUBMITTED (04-MAR-1993) C.A. Batt, Cornell University, 107 Stocking
Hall, Ithaca, NY 14853, USA
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Query Match 57.1% Score 948.6; DB 3; Length 2267;
Best Local Similarity 74.9% Pred. No. 2,5e-180;
Matches 1188; Conservative 0; Mismatches 399; Indels 0; Gaps 0;

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DEFINITION Lactococcus lactis subsp. cremoris chapetonin Groes and chapetonin
ACCESSION AY029215
VERSION AY029215.1 GI:13641349
KEYWORDS Lactococcus lactis subsp. cremoris.
SOURCE Lactococcus lactis subsp. cremoris.
ORGANISM Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
REFERENCE 1 (bases 1 to 2187)
AUTHORS Vogensen, F.K. and Killstrup, M.
JOURNAL Unpublished
TITLE groEL sequence from Lactococcus lactis subsp. cremoris MG1363
REFERENCE 2 (bases 1 to 2187)
AUTHORS Vogensen, F.K. and Killstrup, M.
JOURNAL Direct Submission
TITLE Submitted (04-Apr-2001) Department of Dairy and Food Science, The
JOURNAL Royal Veterinary and Agricultural University, Rolighedsvej 30,

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 ORGANISM  
 Bacteria; Firmicutes; Bacillus/Clostridium group;  
 Bacillus/Staphylococcus group; Bacillus.  
 REFERENCE  
 1 (bases 1 to 2834)  
 Kondo, A. and Yoshida, M.  
 Cpn60/10 from Bacillus strain MS  
 Published only in Database (1999) In press  
 2 (bases 1 to 2834)  
 Kondo, A. and Yoshida, M.  
 Direct Submission  
 Submitted (03-JUN-1999) to the DDBJ/EMBL/GenBank databases. Attilko  
 Kondo, Kobe University, Department of Chemical Science and  
 Engineering, 1-1 Rokkodai-cho, Nada, Kobe, Hyogo 657-8501, Japan  
 (E-mail: kondo@cex.kobe-u.ac.jp, URL: http://www.kobe-u.ac.jp/  
 tel:078-803-6196, fax:078-6206)  
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BASE COUNT 954 a 525 c 668 g 687 t  
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LOCUS	Bacillus stearothermophilus GroES (groES) and GroEL (groEL) genes.
DEFINITION	complete cds.
ACCESSION	L10132
VERSION	L10132.1 GI:289298
KEYWORDS	Chaperonin; groEL gene; groES gene; groEST operon.
SOURCE	Bacillus stearothermophilus.
ORGANISM	Bacillus stearothermophilus Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/staphylococcus group; Bacillus. 1 (bases 1 to 2309) Schoep, U. and Schumann, W. Molecular cloning, sequencing and transcriptional analysis of the groEST operon from Bacillus stearothermophilus J. Bacteriol. 175, 2465-2469 (1993)
JOURNAL	93224474
MEDLINE	location/Qualifiers
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 ACCESSION AF335323.1 GI:13507270  
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 1 (bases 1 to 2156)  
 Gahan, C.G., O'Mahony, J. and Hill, C.  
 Characterization of the groESL operon in Listeria monocytogenes:  
 comparison of two reporter systems (gfp and hly) for evaluating in  
 vivo expression  
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 Gahan, C.G. and Collin, H.  
 Direct Submision  
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 ACCESSION M81132  
 VERSION M81132  
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 SOURCE Bacillus subtilis (strain W168) DNA.  
 ORGANISM Bacillus subtilis  
 Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/staphylococcus group; Bacillus.  
 1 (bases 1 to 2400)  
 Li, M. and Wong, S.-L.  
 Cloning and characterization of the groEL operon from Bacillus subtilis  
 J. Bacteriol. 174, 3981-3992 (1992)  
 JOURNAL MEDLINE 92283733  
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BASE COUNT 757 a 475 c 584 g 584 t

ORIGIN

Query Match 48.6%; Score 807.4; DB 2; Length 2400;  
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 DB 1451 CACTTCACACCTTGTGTGAAACAACTTGGCGGCAACATTCACAGCAAGTGTGATGATG 1510  
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 VERSION M84965.1 GI:143061  
 KEYWORDS ATPase; chaperonin protein; heat shock protein.  
 SOURCE Bacillus subtilis (strain MB11) DNA.  
 ORGANISM Bacillus subtilis  
 Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.  
 REFERENCE 1 (bases 1 to 2525)  
 AUTHORS Schmidt, A., Schlesswohl, M., Voelker, U., Hecker, M. and Schumann, W.  
 TITLE Cloning, sequencing, mapping and transcriptional analysis of the  
 JOURNAL groESL operon from Bacillus subtilis  
 MEDLINE J. Bacteriol. 174, 3993-3999 (1992)  
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BASE COUNT 781 a 504 c 603 g 637 t  
ORIGIN

Query Match 48.68; Score 807.4; DB 2; Length 2525;

Best Local Similarity 68.08; Pred. No. 4.9e-152; Matches 1126; Conservative 0; Mismatches 531; Indels 0; Gaps 0;

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QY 121 ATGTGTTCTTGAAGAAAGCTTTTGTGCTCCTTAAATTAATGACGGGTAACCATTTG 180  
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QY 181 CTAAAGAGATCGAATTTAGATCATTTTGAAGAAACATGGAGCAAAATTTGCTGTGAG 240  
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DB 905 CAATCGAAGCAAAAGAGTATGCTCAGAGTGTGCTGAGTATCTGCTGCTGATGAGAGAG 964  
QY 481 TTGAGAGTATATCTCAGAAAGCATATGAGAGCGTGTGCGCAAGATGGTGTATACATCG 540

DB 965 TCGGAAGCCTTATCGTGAAGCAATGAGCGCGTGTGAGAAACAGAGCGCTTATACATC  
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DB 1025 AAGAGCTTAAGGCTTACACAGCACTGAGCTGAAGTGTGAAGGATGATTTGACCGG 1  
QY 601 GTTACCTCTCAATATACATGCTACAGACATGAAAAAATGCTGACAGCTTGAAGAC 660  
DB 1085 GAAAGCGCTCTTACATGCTGAACGACTGATGATGAAAGCGCTTGTGACAAATC 1144  
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QY 1441 ATGCTGACAGAGTGTGCTGCTGATGATTAAGCAAGCAAGCAAGCAAGTGA 1500  
DB 1925 AAGCTGACAGAGTGTGCTGCTGATGATTAAGCAAGCAAGCAAGCAAGTGA 1984  
QY 1501 TAAACAGATGAGGCTTCAAAATGAGCTGCTGATGATTAATTTGATGACAGAGAG 1560  
DB 1985 TTACAGCTGAGCTTCAAAAGCTGCTGCTGATGATTAATTTGATGACAGAGAG 2044  
QY 1561 CAGTGTGCTTAACTGATACAGCTACGCGAGCGGCAAGCAATGCTGACAGAGTATG 1620

Wed Nov 14 11:59:03 2001

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Page 22

Db 2045 CTGTTGTCCTACACAGCCAGAGAAAACGGTGGCGGCGCAGAGATCCGTGATATGGGCG 2104

Oy 1621 ATCCAGGATGATGGGTGGGATGGCGCGGATAGCCGA 1657

Db 2105 GCATGGCGGTGGTGGATGATGTATATAAGGA 2141

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